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#2

## RAW SEQUENCE LISTING

DATE: 01/28/2002

PATENT APPLICATION: US/10/001,426

TIME: 11:39:27

Input Set : N:\Crf3\RULE60\10001426.raw

Output Set: N:\CRF3\01282002\J001426.raw

## SEQUENCE LISTING

## 1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: HANDA, Hiroshi

3 KAWAGUCHI, Haruma

4 (ii) TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A  
5 PROCESS OF PURIFYING PROTEINS

6 (iii) NUMBER OF SEQUENCES: 13

7 (iv) CORRESPONDENCE ADDRESS:

8 (A) ADDRESSEE: Dike, Bronstein, Roberts &amp; Cushman, LLP

9 (B) STREET: 130 Water Street

10 (C) CITY: Boston

11 (D) STATE: MA

12 (E) COUNTRY: USA

13 (F) ZIP: 02109

14 (v) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: Diskette

16 (B) COMPUTER: IBM Compatible

17 (C) OPERATING SYSTEM: DOS

18 (D) SOFTWARE: FastSEQ Version 1.5

19 (vi) CURRENT APPLICATION DATA:

C--&gt; 20 (A) APPLICATION NUMBER: US/10/001,426

C--&gt; 21 (B) FILING DATE: 02-Nov-2001

22 (C) CLASSIFICATION:

23 (vii) PRIOR APPLICATION DATA:

24 (A) APPLICATION NUMBER: 09/440,597

25 (B) FILING DATE:

26 (viii) ATTORNEY/AGENT INFORMATION:

27 (A) NAME: Corless, Peter F

28 (B) REGISTRATION NUMBER: 33,860

29 (C) REFERENCE/DOCKET NUMBER: 47115

30 (ix) TELECOMMUNICATION INFORMATION:

31 (A) TELEPHONE: 617-523-3400

32 (B) TELEFAX: 617-523-6440

33 (C) TELEX:

34 (2) INFORMATION FOR SEQ ID NO: 1:

35 (i) SEQUENCE CHARACTERISTICS:

36 (A) LENGTH: 6 amino acids

37 (B) TYPE: amino acid

38 (C) STRANDEDNESS: single

39 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: peptide

41 (iii) HYPOTHETICAL: NO

42 (iv) ANTI-SENSE: NO

ENTERED

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43      (v) FRAGMENT TYPE: N-terminal
44      (vi) ORIGINAL SOURCE:
45      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
46          Gly Leu Asp Trp Val Lys
47              1           5
49 (2) INFORMATION FOR SEQ ID NO: 2:
50      (i) SEQUENCE CHARACTERISTICS:
51          (A) LENGTH: 14 amino acids
52          (B) TYPE: amino acid
53          (C) STRANDEDNESS: single
54          (D) TOPOLOGY: linear
55      (ii) MOLECULE TYPE: peptide
56      (iii) HYPOTHETICAL: NO
57      (iv) ANTI-SENSE: NO
58      (v) FRAGMENT TYPE: N-terminal
59      (vi) ORIGINAL SOURCE:
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
61          Ala Ala Gly Glu Gly Pro Ala Leu Tyr Glu Asp Pro Pro Asp
62              1           5           10
64 (2) INFORMATION FOR SEQ ID NO: 3:
65      (i) SEQUENCE CHARACTERISTICS:
66          (A) LENGTH: 10 amino acids
67          (B) TYPE: amino acid
68          (C) STRANDEDNESS: single
69          (D) TOPOLOGY: linear
70      (ii) MOLECULE TYPE: peptide
71      (iii) HYPOTHETICAL: NO
72      (iv) ANTI-SENSE: NO
73      (v) FRAGMENT TYPE: N-terminal
74      (vi) ORIGINAL SOURCE:
75      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
76          Gly Ala Val Ala Glu Asp Gly Asp Glu Leu
77              1           5           10
79 (2) INFORMATION FOR SEQ ID NO: 4:
80      (i) SEQUENCE CHARACTERISTICS:
81          (A) LENGTH: 319 amino acids
82          (B) TYPE: amino acid
83          (C) STRANDEDNESS: single
84          (D) TOPOLOGY: linear
85      (ii) MOLECULE TYPE: peptide
86      (iii) HYPOTHETICAL: NO
87      (iv) ANTI-SENSE: NO
88      (v) FRAGMENT TYPE: N-terminal
89      (vi) ORIGINAL SOURCE:
90      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
91          Met Pro Lys Arg Gly Lys Lys Gly Ala Val Ala Glu Asp Gly Asp Glu
92              1           5           10           15
93          Leu Arg Thr Glu Pro Glu Ala Lys Lys Ser Lys Thr Ala Ala Lys Lys
94              20           25           30

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95   Asn Asp Lys Glu Ala Ala Gly Glu Gly Pro Ala Leu Tyr Glu Asp Pro
96           35                40                45
97   Pro Asp Gln Lys Thr Ser Pro Ser Gly Lys Pro Ala Thr Leu Lys Ile
98           50                55                60
99   Cys Ser Trp Asn Val Asp Gly Leu Arg Ala Trp Ile Lys Lys Lys Gly
100          65                70                75                80
101   Leu Asp Trp Val Lys Glu Glu Asp Ala Pro Asp Ile Leu Cys Leu Gln
102           85                90                95
103   Glu Thr Lys Cys Ser Glu Asn Lys Leu Pro Ala Glu Leu Gln Glu Leu
104           100               105               110
105   Pro Gly Leu Ser His Gln Tyr Trp Ser Ala Pro Ser Asp Lys Glu Gly
106           115               120               125
107   Tyr Ser Gly Val Gly Leu Leu Ser Arg Gln Cys Pro Leu Lys Val Ser
108           130               135               140
109   Tyr Gly Ile Gly Asp Glu Glu His Asp Gln Glu Gly Arg Val Ile Val
110          145               150               155               160
111   Ala Glu Phe Asp Ser Phe Val Leu Val Thr Ala Tyr Val Pro Asn Ala
112           165               170               175
113   Gly Arg Gly Leu Val Arg Leu Glu Tyr Arg Gln Arg Trp Asp Glu Ala
114           180               185               190
115   Phe Arg Lys Phe Leu Lys Gly Leu Ala Ser Arg Lys Pro Leu Val Leu
116           195               200               205
117   Cys Gly Asp Leu Asn Val Ala His Glu Glu Ile Asp Leu Arg Asn Pro
118          210               215               220
119   Lys Gly Asn Lys Lys Asn Ala Gly Phe Thr Pro Gln Glu Arg Gln Gly
120          225               230               235               240
121   Phe Gly Glu Leu Leu Gln Ala Val Pro Leu Ala Asp Ser Phe Arg His
122           245               250               255
123   Leu Tyr Pro Asn Thr Pro Tyr Ala Tyr Thr Phe Trp Thr Tyr Met Met
124           260               265               270
125   Asn Ala Arg Ser Lys Asn Val Gly Trp Arg Leu Asp Tyr Phe Leu Leu
126           275               280               285
127   Ser His Ser Leu Leu Pro Ala Leu Cys Asp Ser Lys Ile Arg Ser Lys
128           290               295               300
129   Ala Leu Gly Ser Asp His Cys Pro Ile Thr Leu Tyr Leu Ala Leu
130          305               310               315

```

132 (2) INFORMATION FOR SEQ ID NO: 5:

133 (i) SEQUENCE CHARACTERISTICS:

134 (A) LENGTH: 31 base pairs

135 (B) TYPE: nucleic acid

136 (C) STRANDEDNESS: single

137 (D) TOPOLOGY: linear

138 (ii) MOLECULE TYPE: cDNA

139 (iii) HYPOTHETICAL: NO

140 (iv) ANTI-SENSE: NO

W--&gt; 141 (v) FRAGMENT TYPE:

142 (vi) ORIGINAL SOURCE:

143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

144 GTCTCTCGAG ATGCCGAAGC GTGGGAAAAA G

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146 (2) INFORMATION FOR SEQ ID NO: 6:
147   (i) SEQUENCE CHARACTERISTICS:
148       (A) LENGTH: 31 base pairs
149       (B) TYPE: nucleic acid
150       (C) STRANDEDNESS: single
151       (D) TOPOLOGY: linear
152   (ii) MOLECULE TYPE: cDNA
153   (iii) HYPOTHETICAL: NO
154   (iv) ANTI-SENSE: NO
W--> 155   (v) FRAGMENT TYPE:
156   (vi) ORIGINAL SOURCE:
157   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
158       ATGCGGATCC TTACAGTGCT AGGTATAGGG T
160 (2) INFORMATION FOR SEQ ID NO: 7:
161   (i) SEQUENCE CHARACTERISTICS:
162       (A) LENGTH: 11 base pairs
163       (B) TYPE: nucleic acid
164       (C) STRANDEDNESS: single
165       (D) TOPOLOGY: linear
166   (ii) MOLECULE TYPE: cDNA
167   (iii) HYPOTHETICAL: NO
168   (iv) ANTI-SENSE: NO
W--> 169   (v) FRAGMENT TYPE:
170   (vi) ORIGINAL SOURCE:
171   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
172       TAACTAATA G
174 (2) INFORMATION FOR SEQ ID NO: 8:
175   (i) SEQUENCE CHARACTERISTICS:
176       (A) LENGTH: 15 base pairs
177       (B) TYPE: nucleic acid
178       (C) STRANDEDNESS: single
179       (D) TOPOLOGY: linear
180   (ii) MOLECULE TYPE: cDNA
181   (iii) HYPOTHETICAL: NO
182   (iv) ANTI-SENSE: NO
W--> 183   (v) FRAGMENT TYPE:
184   (vi) ORIGINAL SOURCE:
185   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
186       ATTGATTGAT CCTAG
188 (2) INFORMATION FOR SEQ ID NO: 9:
189   (i) SEQUENCE CHARACTERISTICS:
190       (A) LENGTH: 32 base pairs
191       (B) TYPE: nucleic acid
192       (C) STRANDEDNESS: single
193       (D) TOPOLOGY: linear
194   (ii) MOLECULE TYPE: cDNA
195   (iii) HYPOTHETICAL: NO
196   (iv) ANTI-SENSE: NO
W--> 197   (v) FRAGMENT TYPE:

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198      (vi) ORIGINAL SOURCE:
199      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
200      ATGCCTCGAG ATGCCAGCCC TGTATGAGGA CC
202 (2) INFORMATION FOR SEQ ID NO: 10:
203      (i) SEQUENCE CHARACTERISTICS:
204          (A) LENGTH: 34 base pairs
205          (B) TYPE: nucleic acid
206          (C) STRANDEDNESS: single
207          (D) TOPOLOGY: linear
208      (ii) MOLECULE TYPE: cDNA
209      (iii) HYPOTHETICAL: NO
210      (iv) ANTI-SENSE: NO
W--> 211      (v) FRAGMENT TYPE:
212      (vi) ORIGINAL SOURCE:
213      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
214      ATGCCTCGAG ATGGATTGGG TAAAGGAAGA AGCC
216 (2) INFORMATION FOR SEQ ID NO: 11:
217      (i) SEQUENCE CHARACTERISTICS:
218          (A) LENGTH: 32 base pairs
219          (B) TYPE: nucleic acid
220          (C) STRANDEDNESS: single
221          (D) TOPOLOGY: linear
222      (ii) MOLECULE TYPE: cDNA
223      (iii) HYPOTHETICAL: NO
224      (iv) ANTI-SENSE: NO
W--> 225      (v) FRAGMENT TYPE:
226      (vi) ORIGINAL SOURCE:
227      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
228      ATGCCTCGAG ATGCCTTCGG ACAAGGAAGG GT
230 (2) INFORMATION FOR SEQ ID NO: 12:
231      (i) SEQUENCE CHARACTERISTICS:
232          (A) LENGTH: 34 base pairs
233          (B) TYPE: nucleic acid
234          (C) STRANDEDNESS: single
235          (D) TOPOLOGY: linear
236      (ii) MOLECULE TYPE: cDNA
237      (iii) HYPOTHETICAL: NO
238      (iv) ANTI-SENSE: NO
W--> 239      (v) FRAGMENT TYPE:
240      (vi) ORIGINAL SOURCE:
241      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
242      ATGCCTCGAG ATGTTTGACT CGTTTGTGCT GGTA
244 (2) INFORMATION FOR SEQ ID NO: 13:
245      (i) SEQUENCE CHARACTERISTICS:
246          (A) LENGTH: 17 amino acids
247          (B) TYPE: amino acid
248          (C) STRANDEDNESS: single
249          (D) TOPOLOGY: linear
250      (ii) MOLECULE TYPE: peptide

```

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10001426.raw

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L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:141 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5  
L:155 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6  
L:169 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7  
L:183 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8  
L:197 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=9  
L:211 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=10  
L:225 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=11  
L:239 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=12